

## Supplementary material

**Table S1.** Demographics and baseline characteristics of the study participants.

Baseline characteristics	Mean	Range
Mothers ( <i>n</i> = 78)		
Age (years)	31 ± 5	19–42
Weight (kg)	74 ± 14	48–109
Height (m)	1.65 ± 0.06	1.52–1.87
Body mass index (kg/m <sup>2</sup> )	27 ± 5	20–39
Babies ( <i>n</i> = 79)		
Birth weight (kg)	3.6 ± 0.5	2.4–4.6
Weight at sample collection (kg)	4.8 ± 0.6	3.3–6.2

Data expressed as mean ± standard deviation.

**Table S2.** Demographics and baseline characteristics of the study participants according to ethnicity.

	Asian	Māori & Pacific Island	New Zealand European	<i>p</i> value
Participants in group ( <i>n</i> )	8	17	53	
Age (years)	30.4 ± 1.2	31.2 ± 1.5	30.7 ± 0.7	0.917
Weight (kg)	58.4 ± 3.1 <sup>a</sup>	80.8 ± 4.2 <sup>b</sup>	74.5 ± 1.6 <sup>b</sup>	<0.001
Height (m)	1.61 ± 0.02	1.65 ± 0.01	1.66 ± 0.01	0.162
Body mass index (kg/m <sup>2</sup> )	22.5 ± 1.1 <sup>a</sup>	29.6 ± 1.5 <sup>b</sup>	27.2 ± 0.6 <sup>b</sup>	0.003
Birth weight (kg)	3.32 ± 0.13	3.63 ± 0.13	3.60 ± 0.06	0.255

Data expressed as mean ± standard error of the mean. Mean values with a different letter differ significantly, *p* < 0.05.

**Table S3.** World Health Organization and New Zealand Ministry of Health classifications of body mass index (kg/m<sup>2</sup>).

	World Health Organisation <sup>1</sup>	New Zealand Ministry of Health <sup>2</sup>		
	All populations	Asian	Māori & Pacific Island	New Zealand European
Underweight	<18.50	<18.50	<18.50	<18.50
Normal	18.50-24.99	18.5-22.9	18.5-26	18.5-25
Overweight	≥25.00	23-27.4	26-32	25-30
Obese	≥30.00	>27.5	>32	>30

<sup>1</sup> Adapted from World Health Organization [1]. <sup>2</sup> Ministry of Health, New Zealand [2].

**Table S4.** Demographics and baseline characteristics of the study participants according to body mass index (BMI) classifications outlined by Ministry of Health, New Zealand.

	Normal	Overweight	Obese	<i>p</i> value
Age (years)	30.3 ± 1.0	31.5 ± 0.8	30.2 ± 1.4	0.559
Weight (kg)	60.4 ± 1.2 <sup>a</sup>	74.7 ± 1.7 <sup>b</sup>	92.0 ± 2.0 <sup>c</sup>	<0.001
Height (cm)	165.0 ± 1.4	165.2 ± 1.0	164.6 ± 1.1	0.943
Baby's weight (kg)	3.52 ± 0.08	3.65 ± 0.09	3.54 ± 0.14	0.592
Participants in BMI category ( <i>n</i> )	27	31	20	

Data expressed as mean ± standard error of the mean. Mean values with a different letter differ significantly, *p* < 0.05.

**Table S5.** Relative abundance of bacteria at genus level in mother's breast milk categorized by body mass index.

	Normal	Overweight	Obese	Benjamini-Hochberg adjusted <i>p</i> value
<i>Actinomyces</i>	0.05 ± 0.04	0.76 ± 0.43	0.31 ± 0.12	0.760
<i>Agrobacterium</i>	0.71 ± 0.43	1.20 ± 1.09	0.06 ± 0.03	0.963
<i>Akkermansia</i>	1.96 ± 0.52	1.86 ± 0.39	1.63 ± 0.57	0.839
<i>Anaerococcus</i>	0.45 ± 0.27	0.10 ± 0.07	0.08 ± 0.05	0.760
<i>Anaerostipes</i>	0.06 ± 0.06	0	0.08 ± 0.08	0.964
<i>Atopobium</i>	0.01 ± 0.00	0.30 ± 0.19	0.74 ± 0.48	0.760
<i>Bacteroidales_S24_7</i>	0.01 ± 0.00	0.04 ± 0.02	0.10 ± 0.06	0.760
<i>Bacteroides</i>	3.07 ± 0.81	2.05 ± 0.51	3.44 ± 0.87	0.760
<i>Barnesiellaceae</i>	0.05 ± 0.05	0.04 ± 0.02	0.08 ± 0.05	0.760
<i>Bifidobacteriaceae</i>	0.09 ± 0.08	0.06 ± 0.03	0.17 ± 0.16	0.760
<i>Bifidobacterium</i>	6.94 ± 1.25	7.52 ± 0.98	7.63 ± 1.99	0.839
<i>Blautia</i>	2.60 ± 0.49	2.70 ± 0.38	2.39 ± 0.43	0.963
<i>Brevundimonas</i>	0.40 ± 0.40	0	0.13 ± 0.12	0.760
<i>Caulobacteraceae</i>	1.41 ± 0.56	1.31 ± 0.79	0.66 ± 0.55	0.760
<i>Christensenella</i>	0.08 ± 0.08	0	0	0.760
<i>Christensenellaceae</i>	0.42 ± 0.15	0.20 ± 0.06	0.23 ± 0.08	0.936
<i>Chryseobacterium</i>	2.03 ± 1.65	3.88 ± 2.13	0.11 ± 0.07	0.760
<i>Clostridiaceae</i>	1.01 ± 0.27	1.01 ± 0.22	0.85 ± 0.26	0.839
<i>Clostridiaceae_Other</i>	0.10 ± 0.06	0.19 ± 0.07	0.17 ± 0.09	0.760
<i>Clostridiales</i>	2.86 ± 0.59	3.40 ± 0.59	2.61 ± 0.45	0.839
<i>Clostridiales_Other</i>	0.46 ± 0.17	0.57 ± 0.13	0.52 ± 0.16	0.760
<i>Clostridium</i>	1.03 ± 0.42	1.47 ± 0.58	0.78 ± 0.38	0.760
<i>Collinsella</i>	1.30 ± 0.29	1.07 ± 0.18	1.13 ± 0.21	0.970
<i>Coprococcus</i>	1.58 ± 0.45	1.93 ± 0.32	1.91 ± 0.55	0.805
<i>Coriobacteriaceae</i>	0.36 ± 0.11	0.38 ± 0.12	0.29 ± 0.14	0.760
<i>Corynebacterium</i>	2.01 ± 0.63	2.21 ± 0.83	7.32 ± 3.20	0.760
<i>Dorea</i>	1.09 ± 0.50	0.59 ± 0.17	0.41 ± 0.21	0.760
<i>Elizabethkingia</i>	4.80 ± 3.32	0	0.056 ± 0.03	0.760
<i>Enterobacteriaceae</i>	0.05 ± 0.04	0.09 ± 0.07	0.42 ± 0.32	0.760
<i>Epulopiscium</i>	0	0.03 ± 0.03	0	0.760
<i>Faecalibacterium</i>	0.96 ± 0.21	1.21 ± 0.24	0.83 ± 0.22	0.848
<i>Finegoldia</i>	0.20 ± 0.13	0.10 ± 0.08	0.05 ± 0.03	0.760
<i>Fusobacterium</i>	0.51 ± 0.29	0.61 ± 0.31	0.50 ± 0.24	0.760
<i>Lachnospira</i>	1.04 ± 0.42	1.15 ± 0.26	0.62 ± 0.19	0.760
<i>Lachnospiraceae</i>	5.07 ± 1.18	6.38 ± 1.11	4.31 ± 0.96	0.839
<i>Lachnospiraceae_Other</i>	0.45 ± 0.22	0.35 ± 0.11	0.59 ± 0.16	0.760
<i>Leucobacter</i>	0.51 ± 0.45	0	0	0.760
<i>Micrococcaceae</i>	0.08 ± 0.08	0	0	0.760
<i>Micrococcus</i>	0.11 ± 0.10	0.03 ± 0.02	0	0.760
<i>Mogibacteriaceae</i>	0.18 ± 0.14	0.05 ± 0.03	0.01 ± 0.01	0.760
<i>Odoribacter</i>	0.07 ± 0.07	0	0	0.760
<i>Oscillospira</i>	0.75 ± 0.25	0.46 ± 0.13	0.56 ± 0.18	0.998
<i>Parabacteroides</i>	0.25 ± 0.10	0.29 ± 0.14	0.36 ± 0.11	0.760
<i>Peptostreptococcus</i>	0.40 ± 0.23	0.27 ± 0.12	0.22 ± 0.14	0.998
<i>Porphyromonas</i>	0.04 ± 0.03	0.21 ± 0.15	0.04 ± 0.04	0.760
<i>Prevotella</i>	0.03 ± 0.02	0.36 ± 0.22	0.19 ± 0.11	0.760
<i>Propionibacterium</i>	0.44 ± 0.17	1.58 ± 1.40	0.48 ± 0.19	0.760
<i>Pseudomonas</i>	0.99 ± 0.82	0.13 ± 0.08	4.56 ± 2.57	0.760
<i>Rikenellaceae</i>	2.72 ± 1.04	2.57 ± 1.02	4.17 ± 1.30	0.760
<i>Roseburia</i>	0.41 ± 0.13	0.63 ± 0.18	0.38 ± 0.17	0.760
<i>Rothia</i>	1.47 ± 0.59	1.84 ± 1.14	2.30 ± 1.11	0.760
<i>Ruminococcaceae</i>	11.4 ± 2.23	13.4 ± 2.09	9.73 ± 1.93	0.760
[ <i>Ruminococcus</i> ]	0.65 ± 0.24	1.49 ± 0.53	0.61 ± 0.22	0.760
<i>Ruminococcus</i>	1.56 ± 0.36	2.46 ± 0.49	1.40 ± 0.34	0.760

<i>Sphingobium</i>	1.21 ± 0.84	0.35 ± 0.11	0.16 ± 0.05	0.839
<i>Sphingomonas</i>	0.47 ± 0.18	0.28 ± 0.12	0.72 ± 0.34	0.760
<i>Streptophyta</i>	0.30 ± 0.16	0.22 ± 0.10	0.08 ± 0.07	0.760
Unassigned	1.53 ± 0.32	1.64 ± 0.23	4.80 ± 1.39	0.839
<i>Veillonella</i>	0.25 ± 0.12	0.19 ± 0.08	0.13 ± 0.07	0.982

Data expressed as mean ± standard error of the mean. Some taxonomy were unable to be identified at the genus level. Square brackets around a genus name indicate a candidate genus.

**Table S6.** Relative abundance of bacteria at genus level in mother's feces categorized according to the body mass index.

	Normal	Overweight	Obese	Benjamini-Hochberg adjusted <i>p</i> value
<i>Actinomyces</i>	0.022 ± 0.02	0	0	0.938
<i>Agrobacterium</i>	0	0.07 ± 0.07	0	0.938
<i>Akkermansia</i>	2.26 ± 0.91	3.74 ± 1.58	2.24 ± 0.83	0.938
<i>Anaerococcus</i>	0	0.05 ± 0.05	0	0.978
<i>Anaerostipes</i>	0.05 ± 0.02	0.09 ± 0.06	0.09 ± 0.03	0.938
<i>Bacteroidales</i>	0.39 ± 0.27	0	0	0.938
<i>Bacteroidales_S24_7</i>	1.13 ± 0.78	0.41 ± 0.31	0.15 ± 0.14	0.938
<i>Bacteroides</i>	17.7 ± 3.59	15.4 ± 2.92	20.5 ± 3.56	0.938
<i>Barnesiellaceae</i>	0.78 ± 0.25	1.04 ± 0.31	1.03 ± 0.30	0.938
<i>Bifidobacterium</i>	2.12 ± 0.55	1.80 ± 0.33	2.40 ± 1.20	0.938
<i>Blautia</i>	2.88 ± 0.74	2.96 ± 0.45	2.27 ± 0.32	0.938
<i>Butyrivimonas</i>	0.14 ± 0.06	0.08 ± 0.03	0.16 ± 0.10	0.938
<i>Caulobacteraceae</i>	0.15 ± 0.10	0.21 ± 0.07	0.33 ± 0.18	0.967
<i>Christensenellaceae</i>	0.56 ± 0.14	0.68 ± 0.16	0.28 ± 0.09	0.938
<i>Clostridiaceae</i>	0.19 ± 0.05	0.42 ± 0.10	0.56 ± 0.19	0.938
<i>Clostridiaceae_Other</i>	0.03 ± 0.01	0.04 ± 0.01	0.07 ± 0.06	0.938
<i>Clostridiales</i>	5.28 ± 0.86	5.75 ± 0.72	3.35 ± 0.62	0.938
<i>Clostridiales_Other</i>	0.59 ± 0.13	1.24 ± 0.25	0.66 ± 0.10	0.938
<i>Clostridium</i>	0.30 ± 0.05	0.35 ± 0.05	0.31 ± 0.04	0.938
<i>Collinsella</i>	0.97 ± 0.34	0.76 ± 0.13	0.53 ± 0.12	0.938
<i>Coprococcus</i>	2.68 ± 0.41	3.27 ± 0.70	2.25 ± 0.30	0.938
<i>Coriobacteriaceae</i>	0.29 ± 0.08	0.42 ± 0.11	0.26 ± 0.07	0.938
<i>Dorea</i>	0.49 ± 0.10	1.04 ± 0.28	0.60 ± 0.09	0.938
<i>Eggerthella</i>	0.05 ± 0.02	0.03 ± 0.01	0.08 ± 0.05	0.938
<i>Enterobacteriaceae</i>	0.11 ± 0.07	0.07 ± 0.04	0	0.938
<i>Epulopiscium</i>	0.21 ± 0.21	0	0	0.938
<i>Faecalibacterium</i>	1.70 ± 0.43	1.42 ± 0.32	1.68 ± 0.41	0.938
<i>Finegoldia</i>	0.15 ± 0.05	0.19 ± 0.07	0.14 ± 0.06	0.938
<i>Fusobacterium</i>	0.01 ± 0.01	1.45 ± 1.43	0.01 ± 0.01	0.938
<i>Lachnospira</i>	1.89 ± 0.57	1.75 ± 0.61	1.31 ± 0.63	0.938
<i>Lachnospiraceae</i>	5.11 ± 0.96	6.65 ± 1.24	7.01 ± 1.25	0.938
<i>Lachnospiraceae_Other</i>	0.46 ± 0.09	0.52 ± 0.10	0.50 ± 0.11	0.978
<i>Mogibacteriaceae</i>	0.04 ± 0.02	0.08 ± 0.02	0.05 ± 0.03	0.938
<i>Odoribacter</i>	0.13 ± 0.03	0.16 ± 0.05	0.27 ± 0.09	0.938
<i>Oscillospira</i>	0.89 ± 0.20	0.94 ± 0.31	0.58 ± 0.12	0.941
<i>Parabacteroides</i>	1.92 ± 0.66	1.34 ± 0.36	1.61 ± 0.42	0.938
<i>Paraprevotella</i>	0.20 ± 0.16	0.13 ± 0.08	1.15 ± 0.98	0.938
<i>Porphyromonas</i>	0.04 ± 0.03	0.01 ± 0.01	0.01 ± 0.01	0.938
<i>Prevotella</i>	3.50 ± 2.03	0.50 ± 0.24	0.85 ± 0.55	0.938
<i>Rikenellaceae</i>	3.22 ± 0.94	3.03 ± 0.63	2.94 ± 0.72	0.967
<i>Rikenellaceae_Other</i>	0	0.03 ± 0.03	0	0.938
<i>Roseburia</i>	0.66 ± 0.53	0.59 ± 0.18	0.72 ± 0.33	0.938
<i>Ruminococcaceae</i>	22.2 ± 3.80	17.6 ± 3.08	25.9 ± 4.48	0.938
[ <i>Ruminococcus</i> ]	0.71 ± 0.18	1.78 ± 0.86	0.71 ± 0.18	0.967
<i>Ruminococcus</i>	0.29 ± 0.81	3.79 ± 0.95	3.80 ± 0.79	0.938
<i>Sphingomonas</i>	0.03 ± 0.02	0.01 ± 0.01	0.01 ± 0.01	0.938

<i>Sutterella</i>	0.12 ± 0.08	0.08 ± 0.07	0.02 ± 0.01	0.938
Unassigned	2.25 ± 0.25	2.23 ± 0.22	1.86 ± 0.16	0.938
<i>Veillonella</i>	1.26 ± 0.47	1.54 ± 0.50	2.40 ± 1.48	0.980

Data expressed as mean ± standard error of the mean. Some taxonomy were unable to be identified at the genus level. Square brackets around a genus name indicate a candidate genus.

**Table S7.** Relative abundance of bacteria at genus level in infant's feces categorized according to the mother's body mass index.

	Normal	Overweight	Obese	Benjamini-Hochberg adjusted <i>p</i> value
<i>Actinomyces</i>	1.31 ± 1.26	0.05 ± 0.03	1.67 ± 1.58	0.965
<i>Agrobacterium</i>	0	0.12 ± 0.08	0.01 ± 0.01	0.965
<i>Akkermansia</i>	0.12 ± 0.11	0.05 ± 0.03	0.01 ± 0.01	0.965
<i>Bacteroides</i>	19.9 ± 5.39	12.4 ± 4.03	24.8 ± 7.31	0.965
<i>Bifidobacterium</i>	45.5 ± 6.75	52.7 ± 6.29	32.8 ± 7.98	0.965
<i>Blautia</i>	0.65 ± 0.44	0.32 ± 0.17	0.08 ± 0.04	0.965
<i>Caulobacteraceae</i>	0.45 ± 0.45	2.59 ± 1.98	0.02 ± 0.02	0.965
<i>Clostridiaceae</i>	3.42 ± 2.75	3.34 ± 2.11	3.41 ± 3.25	0.965
<i>Clostridiaceae</i> _Other	0.03 ± 0.03	0.02 ± 0.01	0.01 ± 0.00	0.965
<i>Clostridiales</i>	0.78 ± 0.60	0.18 ± 0.09	0.13 ± 0.05	0.965
<i>Clostridiales</i> _Other	0.09 ± 0.06	0.04 ± 0.01	0.08 ± 0.04	0.965
<i>Clostridium</i>	5.79 ± 3.48	11.8 ± 5.23	17.6 ± 8.03	0.965
<i>Collinsella</i>	3.50 ± 1.93	1.50 ± 0.55	3.12 ± 1.76	0.965
<i>Coprococcus</i>	0.29 ± 0.18	0.21 ± 0.11	0.08 ± 0.04	0.965
<i>Coriobacteriaceae</i>	0.08 ± 0.05	0.79 ± 0.63	0.02 ± 0.01	0.965
<i>Dorea</i>	0.95 ± 0.93	0.23 ± 0.19	0.10 ± 0.08	0.988
<i>Eggerthella</i>	0.19 ± 0.10	0.05 ± 0.02	0.12 ± 0.07	0.965
<i>Enterobacteriaceae</i>	0.25 ± 0.08	0.40 ± 0.12	0.36 ± 0.11	0.965
<i>Faecalibacterium</i>	0.09 ± 0.06	0.06 ± 0.04	0.02 ± 0.01	0.965
<i>Finegoldia</i>	0.05 ± 0.05	0.02 ± 0.01	0.02 ± 0.02	0.965
<i>Fusobacterium</i>	0.65 ± 0.64	0.02 ± 0.01	0.01 ± 0.01	0.965
<i>Lachnospiraceae</i>	1.49 ± 0.59	0.25 ± 0.12	2.11 ± 1.41	0.965
<i>Lachnospiraceae</i> _Other	0.07 ± 0.02	0.03 ± 0.01	1.78 ± 1.72	0.965
<i>Megasphaera</i>	0	0.19 ± 0.14	0.10 ± 0.10	0.965
<i>Odoribacter</i>	0.09 ± 0.09	0.04 ± 0.04	0	0.965
<i>Oscillospira</i>	0.33 ± 0.19	0.08 ± 0.07	0.27 ± 0.25	0.965
<i>Parabacteroides</i>	1.71 ± 0.89	3.44 ± 2.29	0.99 ± 0.54	0.965
<i>Peptostreptococcus</i>	0.06 ± 0.05	0.01 ± 0.01	0.11 ± 0.11	0.965
<i>Porphyromonas</i>	0	0	0.15 ± 0.14	0.965
<i>Prevotella</i>	0.05 ± 0.02	0.02 ± 0.01	0.26 ± 0.22	0.965
<i>Pseudoramibacter</i>	0	0.16 ± 0.13	0	0.965
<i>Rikenellaceae</i>	0.59 ± 0.33	0.36 ± 0.24	0.04 ± 0.03	0.965
<i>Ruminococcaceae</i>	0.95 ± 0.44	2.27 ± 1.62	0.15 ± 0.04	0.979
[ <i>Ruminococcus</i> ]	3.89 ± 1.64	0.76 ± 0.36	5.35 ± 4.56	0.965
<i>Ruminococcus</i>	0.21 ± 0.13	0.18 ± 0.10	0.09 ± 0.03	0.965
<i>Sphingomonas</i>	0.50 ± 0.49	0.02 ± 0.02	0	0.965
Unassigned	2.70 ± 0.42	2.70 ± 0.48	2.43 ± 0.49	0.965
<i>Veillonella</i>	0.40 ± 0.26	0.40 ± 0.25	0.30 ± 0.18	0.979

Data expressed as mean ± standard error of the mean. Some taxonomy were unable to be identified at the genus level. Square brackets around a genus name indicate a candidate genus.

**Table S8.** Relative abundance of bacteria at genus level in mother's breast milk categorized according to the mode of delivery.

	Cesarean	Vaginal	Benjamini-Hochberg adjusted <i>p</i> value
<i>Actinomyces</i>	0.10 ± 0.05	0.46 ± 0.22	1.000
<i>Agrobacterium</i>	0.05 ± 0.04	0.88 ± 0.55	1.000
<i>Akkermansia</i>	1.77 ± 0.69	1.85 ± 0.30	1.000
<i>Anaerococcus</i>	0.03 ± 0.03	0.26 ± 0.12	1.000
<i>Anaerostipes</i>	0	0.05 ± 0.04	1.000
<i>Atopobium</i>	0.09 ± 0.07	0.36 ± 0.18	1.000
<i>Bacteroidales_S24_7</i>	0.03 ± 0.02	0.05 ± 0.02	1.000
<i>Bacteroides</i>	1.59 ± 0.57	3.03 ± 0.49	1.000
<i>Barnesiellaceae</i>	0	0.06 ± 0.03	1.000
<i>Bifidobacteriaceae</i>	0.19 ± 0.15	0.08 ± 0.05	1.000
<i>Bifidobacterium</i>	7.79 ± 2.87	7.25 ± 0.71	1.000
<i>Blautia</i>	2.00 ± 0.54	2.71 ± 0.28	1.000
<i>Brevundimonas</i>	0	0.21 ± 0.17	1.000
<i>Caulobacteraceae</i>	1.94 ± 1.53	1.01 ± 0.34	1.000
<i>Christensenella</i>	0	0.03 ± 0.03	1.000
<i>Christensenellaceae</i>	0.18 ± 0.10	0.31 ± 0.07	1.000
<i>Chryseobacterium</i>	3.39 ± 3.11	2.00 ± 1.04	1.000
<i>Clostridiaceae</i>	0.71 ± 0.27	1.03 ± 0.17	1.000
<i>Clostridiaceae_Other</i>	0.16 ± 0.11	0.15 ± 0.05	1.000
<i>Clostridiales</i>	2.78 ± 0.77	3.06 ± 0.37	1.000
<i>Clostridiales_Other</i>	0.43 ± 0.19	0.54 ± 0.10	1.000
<i>Clostridium</i>	0.67 ± 0.35	1.24 ± 0.34	1.000
<i>Collinsella</i>	1.17 ± 0.29	1.17 ± 0.15	1.000
<i>Coprococcus</i>	2.03 ± 0.59	1.75 ± 0.24	1.000
<i>Coriobacteriaceae</i>	0.15 ± 0.07	0.39 ± 0.08	1.000
<i>Corynebacterium</i>	4.15 ± 3.75	3.32 ± 0.82	1.000
<i>Dorea</i>	0.39 ± 0.15	0.79 ± 0.24	1.000
<i>Elizabethkingia</i>	0.04 ± 0.03	2.07 ± 1.44	1.000
<i>Enterobacteriaceae</i>	0.61 ± 0.46	0.06 ± 0.03	1.000
<i>Epulopiscium</i>	0	0.02 ± 0.01	1.000
<i>Faecalibacterium</i>	1.21 ± 0.44	0.98 ± 0.13	1.000
<i>Finegoldia</i>	0	0.15 ± 0.07	1.000
<i>Fusobacterium</i>	0.66 ± 0.41	0.52 ± 0.19	1.000
<i>Lachnospira</i>	0.89 ± 0.43	0.99 ± 0.21	1.000
<i>Lachnospiraceae</i>	5.28 ± 1.49	5.41 ± 0.72	1.000
<i>Lachnospiraceae_Other</i>	0.35 ± 0.16	0.47 ± 0.11	1.000
<i>Leucobacter</i>	0.86 ± 0.86	0.03 ± 0.03	1.000
<i>Micrococcaceae</i>	0	0.04 ± 0.04	1.000
<i>Micrococcus</i>	0.02 ± 0.02	0.06 ± 0.05	1.000
<i>Mogibacteriaceae</i>	0	0.10 ± 0.06	1.000
<i>Odoribacter</i>	0	0.03 ± 0.03	1.000
<i>Oscillospira</i>	0.68 ± 0.27	0.57 ± 0.12	1.000
<i>Parabacteroides</i>	0.19 ± 0.12	0.32 ± 0.08	1.000
<i>Peptostreptococcus</i>	0.03 ± 0.02	0.36 ± 0.12	1.000
<i>Porphyromonas</i>	0.06 ± 0.06	0.11 ± 0.07	1.000
<i>Prevotella</i>	0.13 ± 0.08	0.22 ± 0.11	1.000
<i>Propionibacterium</i>	0.12 ± 0.05	1.06 ± 0.67	1.000
<i>Pseudomonas</i>	1.18 ± 1.01	1.68 ± 0.88	1.000
<i>Rikenellaceae</i>	2.28 ± 1.12	3.20 ± 0.73	1.000
<i>Roseburia</i>	0.40 ± 0.20	0.51 ± 0.11	1.000
<i>Rothia</i>	0.46 ± 0.17	2.13 ± 0.68	1.000
<i>Ruminococcaceae</i>	13.0 ± 3.48	11.5 ± 1.31	1.000
[ <i>Ruminococcus</i> ]	1.68 ± 1.06	0.81 ± 0.17	1.000
<i>Ruminococcus</i>	2.32 ± 0.87	1.77 ± 0.24	1.000

<i>Sphingobium</i>	0.77 ± 0.51	0.57 ± 0.35	1.000
<i>Sphingomonas</i>	0.64 ± 0.36	0.42 ± 0.12	1.000
<i>Streptophyta</i>	0.05 ± 0.05	0.24 ± 0.08	1.000
Unassigned	2.99 ± 1.40	2.30 ± 0.41	1.000
<i>Veillonella</i>	0.23 ± 0.19	0.20 ± 0.05	1.000

Data expressed as mean ± standard error of the mean. Some taxonomy were unable to be identified at the genus level. Square brackets around a genus name indicate a candidate genus.

**Table S9.** Relative abundance of bacteria at genus level in mother's feces categorized according to the mode of delivery.

	Cesarean	Vaginal	Benjamini-Hochberg adjusted <i>p</i> value
<i>Actinomyces</i>	0	0.01 ± 0.01	0.935
<i>Agrobacterium</i>	0	0.04 ± 0.04	0.935
<i>Akkermansia</i>	2.86 ± 1.23	2.83 ± 0.84	0.935
<i>Anaerococcus</i>	0	0.03 ± 0.03	0.935
<i>Anaerostipes</i>	0.19 ± 0.13	0.05 ± 0.01	0.935
<i>Bacteroidales</i>	0	0.17 ± 0.12	0.964
<i>Bacteroidales_S24_7</i>	0.85 ± 0.66	0.54 ± 0.34	0.935
<i>Bacteroides</i>	16.8 ± 3.70	17.7 ± 2.21	0.935
<i>Barnesiellaceae</i>	0.73 ± 0.25	0.99 ± 0.20	0.964
<i>Bifidobacterium</i>	1.60 ± 0.57	2.17 ± 0.45	0.935
<i>Blautia</i>	3.34 ± 0.92	2.63 ± 0.34	0.935
<i>Butyrivimonas</i>	0.04 ± 0.02	0.14 ± 0.04	0.935
<i>Caulobacteraceae</i>	0.37 ± 0.24	0.19 ± 0.06	0.935
<i>Christensenellaceae</i>	0.38 ± 0.16	0.56 ± 0.10	0.935
<i>Clostridiaceae</i>	0.62 ± 0.22	0.32 ± 0.06	0.935
<i>Clostridiaceae_Other</i>	0.03 ± 0.02	0.05 ± 0.02	0.935
<i>Clostridiales</i>	5.03 ± 1.09	4.95 ± 0.50	0.973
<i>Clostridiales_Other</i>	1.29 ± 0.47	0.76 ± 0.10	0.935
<i>Clostridium</i>	0.43 ± 0.08	0.29 ± 0.03	0.935
<i>Collinsella</i>	0.52 ± 0.11	0.83 ± 0.16	0.935
<i>Coprococcus</i>	2.73 ± 0.45	2.82 ± 0.38	0.935
<i>Coriobacteriaceae</i>	0.41 ± 0.11	0.33 ± 0.06	0.935
<i>Dorea</i>	0.79 ± 0.19	0.72 ± 0.14	0.935
<i>Eggerthella</i>	0.03 ± 0.01	0.06 ± 0.02	0.964
<i>Enterobacteriaceae</i>	0.01 ± 0.00	0.08 ± 0.04	0.935
<i>Epulopiscium</i>	0	0.09 ± 0.09	0.935
<i>Faecalibacterium</i>	1.93 ± 0.57	1.51 ± 0.24	0.935
<i>Finegoldia</i>	0.12 ± 0.07	0.17 ± 0.04	0.935
<i>Fusobacterium</i>	0	0.70 ± 0.68	0.935
<i>Lachnospira</i>	1.77 ± 0.84	1.67 ± 0.38	0.935
<i>Lachnospiraceae</i>	9.68 ± 2.14	5.43 ± 0.64	0.935
<i>Lachnospiraceae_Other</i>	0.70 ± 0.17	0.45 ± 0.06	0.935
<i>Mogibacteriaceae</i>	0.04 ± 0.02	0.06 ± 0.02	0.935
<i>Odoribacter</i>	0.17 ± 0.05	0.18 ± 0.04	0.964
<i>Oscillospira</i>	0.65 ± 0.14	0.87 ± 0.17	0.964
<i>Parabacteroides</i>	1.05 ± 0.32	1.74 ± 0.35	0.935
<i>Paraprevotella</i>	0.23 ± 0.17	0.46 ± 0.32	0.935
<i>Porphyromonas</i>	0.01 ± 0.01	0.03 ± 0.01	0.935
<i>Prevotella</i>	1.13 ± 0.79	1.76 ± 0.89	0.997
<i>Rikenellaceae</i>	3.78 ± 0.96	2.92 ± 0.50	0.935
<i>Rikenellaceae_Other</i>	0	0.02 ± 0.01	0.964
<i>Roseburia</i>	0.53 ± 0.27	0.68 ± 0.26	0.935
<i>Ruminococcaceae</i>	18.0 ± 3.75	22.1 ± 2.48	0.935
[ <i>Ruminococcus</i> ]	1.22 ± 0.52	1.11 ± 0.41	0.935
<i>Ruminococcus</i>	5.61 ± 1.51	3.01 ± 0.51	0.935
<i>Sphingomonas</i>	0.02 ± 0.01	0.02 ± 0.01	0.935

<i>Sutterella</i>	0.17 ± 0.14	0.06 ± 0.03	0.935
Unassigned	2.19 ± 0.26	2.13 ± 0.15	0.935
<i>Veillonella</i>	2.76 ± 1.95	1.42 ± 0.36	0.964

Data expressed as mean ± standard error of the mean. Some taxonomy were unable to be identified at the genus level. Square brackets around a genus name indicate a candidate genus.

**Table S10.** Relative abundance of bacteria in infant's feces at genus level categorized according to the mode of delivery.

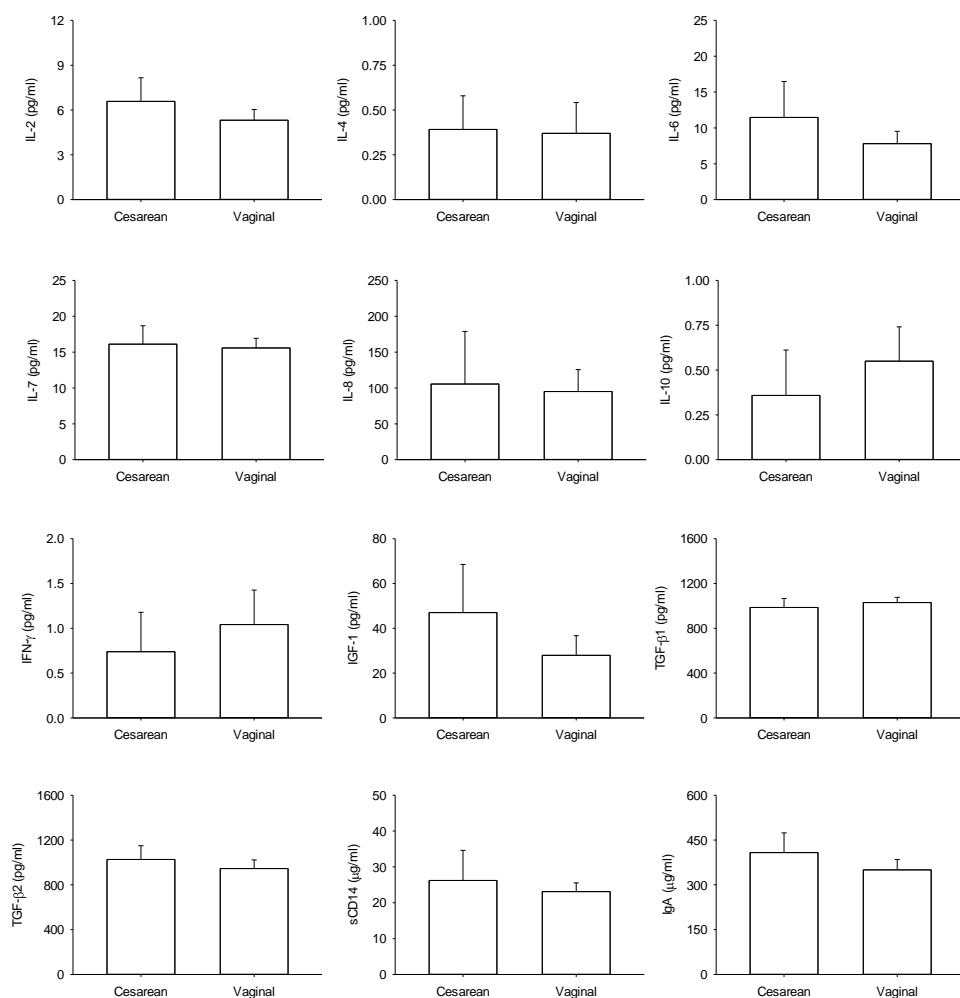
	<b>Cesarean</b>	<b>Vaginal</b>	<b>Benjamini-Hochberg adjusted <i>p</i> value</b>
<i>Actinomyces</i>	2.74 ± 2.61	0.52 ± 0.48	0.848
<i>Agrobacterium</i>	0.13 ± 0.12	0.03 ± 0.03	0.557
<i>Akkermansia</i>	0.08 ± 0.07	0.06 ± 0.05	0.848
<i>Anaerotruncus</i>	0	0.02 ± 0.02	0.848
<i>Bacteroides</i>	6.28 ± 5.38	20.6 ± 3.51	0.104
<i>Bifidobacterium</i>	41.7 ± 10.8	45.9 ± 4.36	0.848
<i>Blautia</i>	0.98 ± 0.88	0.25 ± 0.10	0.850
<i>Caulobacteraceae</i>	0.15 ± 0.15	1.40 ± 0.96	0.614
<i>Clostridiaceae</i>	6.13 ± 4.77	2.82 ± 1.53	0.104
<i>Clostridiaceae_Other</i>	0.01 ± 0.01	0.02 ± 0.01	0.848
<i>Clostridiales</i>	0.18 ± 0.10	0.42 ± 0.26	0.947
<i>Clostridiales_Other</i>	0.04 ± 0.02	0.06 ± 0.03	0.848
<i>Clostridium</i>	18.6 ± 9.36	9.55 ± 3.26	0.557
<i>Collinsella</i>	0.02 ± 0.02*	3.15 ± 1.00*	<0.001
<i>Coprococcus</i>	0.09 ± 0.06	0.23 ± 0.09	0.850
<i>Coriobacteriaceae</i>	0.01 ± 0.01	0.42 ± 0.30	0.532
<i>Dorea</i>	0.52 ± 0.43	0.44 ± 0.40	0.782
<i>Eggerthella</i>	0.03 ± 0.02	0.14 ± 0.05	0.532
<i>Enterobacteriaceae</i>	0.52 ± 0.16	0.30 ± 0.07	0.484
<i>Faecalibacterium</i>	0.11 ± 0.08	0.05 ± 0.03	0.848
<i>Finegoldia</i>	0	0.03 ± 0.02	0.490
<i>Fusobacterium</i>	1.36 ± 1.32	0.01 ± 0.01	0.312
<i>Lachnospiraceae</i>	1.41 ± 0.84	1.10 ± 0.41	0.782
<i>Lachnospiraceae_Other</i>	0.10 ± 0.04	0.56 ± 0.52	0.490
<i>Megasphaera</i>	0	0.12 ± 0.07	0.848
<i>Odoribacter</i>	0	0.06 ± 0.04	0.615
<i>Oscillospira</i>	0.01 ± 0.01	0.26 ± 0.12	0.848
<i>Parabacteroides</i>	5.16 ± 5.15	1.61 ± 0.51	0.615
<i>Peptostreptococcus</i>	0	0.06 ± 0.04	0.848
<i>Porphyromonas</i>	0	0.05 ± 0.04	0.557
<i>Prevotella</i>	0.01 ± 0.00	0.11 ± 0.07	0.848
<i>Pseudoramibacter</i>	0	0.08 ± 0.06	0.848
<i>Rikenellaceae</i>	0.01 ± 0.00	0.43 ± 0.18	0.850
<i>Ruminococcaceae</i>	0.73 ± 0.55	1.38 ± 0.79	0.848
[ <i>Ruminococcus</i> ]	7.88 ± 6.63	2.02 ± 0.75	0.507
<i>Ruminococcus</i>	0.28 ± 0.22	0.14 ± 0.06	0.848
<i>Sphingomonas</i>	0	0.22 ± 0.21	0.848
Unassigned	3.05 ± 0.97	2.55 ± 0.26	0.848
<i>Veillonella</i>	0.69 ± 0.34	0.31 ± 0.15	0.532

Data expressed as mean ± standard error of the mean. Some taxonomy were unable to be identified at the genus level. Square brackets around a genus name indicate a candidate genus. Mean values marked with \* differ significantly,  $p < 0.05$ .

**Table S11.** Summary of immune modulatory proteins analyzed, their potential impact on infant health, and maternal diet and lifestyle influences affecting their concentrations in breast milk.

<b>Breast milk proteins analyzed</b>	<b>Potential role</b>	<b>Reference</b>
Interleukin 2	Role in T cell differentiation	[3]
	Diet can impact the amount present in breast milk	[4]
Interleukin 4	Role in allergies and immunoglobulin (Ig) E production	[5]
	Higher in milk when maternal allergies are present	[6]
	Higher in mature milk of smokers	[7]
Interleukin 6	Predominant cytokine in milk	[7]
	Has a role in the differentiation of IgA producing cells	[8]
	Higher in mature milk of smokers	[7]
Interleukin 7	Lower in milk when maternal allergies are present	[7]
	Regulatory cytokine that can cross the intestinal wall and influence thymic development in infants	[9]
Interleukin 8	Role in neutrophil recruitment	[10]
	High levels indicate subclinical breast inflammation leading to poor infant growth	[11]
	High amounts in mature milk of mothers who had pre-eclampsia	[12]
	Decreased in milk when maternal rhinitis is present	
Interleukin 10	Plays a role in oral tolerance	
	Involved in IgA synthesis	
Interferon $\gamma$	Has a critical role in innate and adaptive immunity	[13]
	Recruits macrophages	[13]
	Higher in mature milk of smokers	[7]
	Increases as milk matures	[4]
Insulin-like growth factor 1	Remains low in infants that develop atopy	[14]
	High amounts in milk associated with high weight gain in infants	[15]
Transforming growth factor $\beta$ 1	Promotes functional development of the gastrointestinal mucosa	[16]
	Plays a role in oral tolerance	[17]
Transforming growth factor $\beta$ 2	Predominant cytokine in milk	[6]
	Lower in milk when maternal allergies are present	[18]
	Lower in milk with increased maternal body mass index (BMI), but not significant	[19]
	Milk concentrations correlate with maternal polyunsaturated fatty acid consumption	[18]
Soluble cluster of differentiation 14	Enhances cellular response to microbial components	[20]
	Lower amounts in human milk as it matures	[19]
	Higher amounts in milk are associated with bifidobacteria and staphylococci	[19]
	Low amounts in milk is associated with high BMI	[19]
Immunoglobulin A	Binds microbial antigens	[8,19]
	Enhances phagocytosis	[8]
	Promotes normal microbial colonization in the gut	[8]





**Figure S1.** Immune related proteins in mother's breast milk categorized according to the mode of delivery of infants. Data expressed as mean  $\pm$  standard error of the mean. IL – Interleukin, IFN – Interferon, IGF – Insulin-like growth factor, TGF – Transforming growth factor, sCD – Soluble cluster of differentiation, Ig – Immunoglobulin.

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